

WHAT IS CLAIMED IS:

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1. An isolated nucleic acid encoding a polypeptide monomer of a pH sensitive potassium channel, the monomer:
- 5 (i) having a calculated molecular weight of between 120-156 kDa;
(ii) having a unit conductance of approximately 80-120 pS when the monomer is in a functional tetrameric form of a potassium channel and is expressed in a *Xenopus* oocyte;
- 10 (iii) having increased activity above approximately intracellular pH of 7.1; and
(iv) specifically binding to polyclonal antibodies generated against SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16, or SEQ ID NO:18.

15 2. An isolated nucleic acid of claim 1, wherein the nucleic acid encodes mSlo3.

3. An isolated nucleic acid of claim 1, wherein the nucleic acid encodes hSlo3.

20 4. An isolated nucleic acid of claim 1, wherein the nucleic acid encodes SEQ ID NO:1.

25 5. An isolated nucleic acid of claim 1, wherein the nucleic acid encodes SEQ ID NO:16 or 18.

6. An isolated nucleic acid of claim 1, wherein the nucleic acid selectively hybridizes under moderate stringency hybridization conditions to SEQ ID NO:2.

7. An isolated nucleic acid of claim 1, wherein the nucleic acid selectively hybridizes under moderate stringency hybridization conditions to SEQ ID NO:4, SEQ ID NO:17, or SEQ ID NO:19.

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8. An isolated nucleic acid sequence of claim 1, wherein the nucleic acid has a nucleotide sequence of SEQ ID NO:2.

5 9. An isolated nucleic acid sequence of claim 1, wherein the nucleic acid has a nucleotide sequence of SEQ ID NO:4, SEQ ID NO:17, or SEQ ID NO:19.

10 10. An isolated nucleic acid of claim 1, wherein the nucleic acid is amplified by primers that selectively hybridize under stringent hybridization conditions to the same sequence as the primer sets selected from the group consisting of:

CTCGAACTCCCTAAAATCTTACAGAT (SEQ ID NO:8) and
TTCCGTTGAGCCAGGGGTCACCAGAATT (SEQ ID NO:9);
TCTGCTTTGTGAAGCTAAATCT (SEQ ID NO:10) and
TTTCAAAGCCTCTTTAGCGGTAA (SEQ ID NO:11); and
TTATGCCTGGATCTGCACTCTACATG (SEQ ID NO:12) and
15 ATAGTTTCCGTCTACTACCGAAA (SEQ ID NO:13).

20 11. An isolated nucleic acid of claim 1, wherein the nucleic acid is amplified by primers that selectively hybridize under stringent hybridization conditions to the same sequence as the primer sets selected from the group consisting of:

GGCAGCGCTCATTCTTTCCTCCTT (SEQ ID NO:14) and
TGCCCAAACCTCAACCCAAAATA (SEQ ID NO:15).

25 12. An isolated nucleic acid encoding at least 15 contiguous amino acids from a pH sensitive potassium channel polypeptide monomer, said monomer having an amino acid sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16, SEQ ID NO:18 and conservatively modified variants thereof.

30 13. The isolated nucleic acid of claim 12, wherein said nucleic acid encodes a pH sensitive potassium channel polypeptide monomer having:

(i) a unit conductance of 80-120 pS when the monomer is in a functional tetrameric form of a potassium channel and is expressed in a *Xenopus* oocyte; and

(ii) a molecular weight of between 120-156 kDa; and

(iii) increased activity above an intracellular pH of 7.1;

wherein said nucleic acid either:

(i) selectively hybridizes under moderate stringency hybridization conditions to a nucleotide sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:17,

5 SEQ ID NO:19; or

(ii) encodes a protein which could be encoded by a nucleic acid that selectively hybridizes under moderate stringency hybridization conditions to a nucleotide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:17, SEQ ID NO:19.

10 14. An isolated nucleic acid encoding a polypeptide monomer of a pH sensitive potassium channel, the sequence:

(i) encoding a monomer having a core domain that has greater than 60% amino acid sequence identity to amino acids 35-641 of a Slo3 core domain as measured using a sequence comparison algorithm; and

15 (ii) specifically binding to polyclonal antibodies raised against the core domain of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16, or SEQ ID NO:18.

15 15. An isolated nucleic acid of claim 14, wherein the Slo3 has a sequence of SEQ ID NO:1.

16 16. An isolated nucleic acid of claim 14, wherein the Slo3 has a sequence of SEQ ID NO:16 or SEQ ID NO:18.

25 17. An isolated polypeptide monomer of a pH sensitive potassium channel, the monomer:

(i) having a calculated molecular weight of between 120-156 kDa;

(ii) having a unit conductance of approximately 80-120 pS when the monomer is in a functional tetrameric form of a potassium channel and is expressed in a *Xenopus* oocyte;

30 (iii) having increased activity above approximately intracellular pH of 7.1; and

(iv) specifically binding to polyclonal antibodies generated against SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16 OR SEQ ID NO:18.

18. An isolated monomer of claim 17, wherein the monomer has an amino acid sequence of mSlo3.

5 19. An isolated monomer of claim 17, wherein the monomer has an amino acid sequence of hSlo3.

20. An isolated monomer of claim 17, wherein the monomer has an amino acid sequence of SEQ ID NO:1.

10 21. An isolated monomer of claim 17, wherein the monomer has an amino acid sequence of SEQ ID NO:16 or SEQ ID NO:18.

22. An antibody that selectively binds to mSlo3.

15 23. An antibody of claim 22, wherein the mSlo3 has an amino acid sequence of SEQ ID NO:1.

24. An antibody that selectively binds to hSlo3.

20 25. An antibody of claim 24, wherein the hSlo3 has an amino acid sequence of SEQ ID NO:16 or SEQ ID NO:18.

26. An expression vector comprising a nucleic acid encoding a polypeptide monomer of a pH sensitive potassium channel, the monomer:

25 (i) having a calculated molecular weight of between 120-156 kDa;

(ii) having a unit conductance of approximately 80-120 pS when

the monomer is in a functional tetrameric form of a potassium channel and is expressed in a *Xenopus* oocyte;

(iii) having increased activity above approximately intracellular pH

30 of 7.1; and

(iv) specifically binding to polyclonal antibodies generated against SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16, or SEQ ID NO:18.

27. A host cell transfected with the vector of claim 26.

28. A method for identifying a compound that increases or decreases ion flux through a pH sensitive potassium channel, the method comprising the steps of:

(i) contacting the compound with a eukaryotic host cell or cell membrane in which has been expressed a pH sensitive potassium channel monomer polypeptide:

(a) having a calculated molecular weight of between 120-156 kDa;

(b) having a unit conductance of approximately 80-120 pS when the monomer is in the functional tetrameric form of a potassium channel and is expressed in a *Xenopus* oocyte; and

(c) specifically binding to polyclonal antibodies generated against SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16 or SEQ ID NO:18; and

(ii) determining the functional effect of the compound upon the cell or cell membrane expressing the pH sensitive potassium channel.

29. A method of claim 28, wherein the increased or decreased flux of ions is determined by measuring whole cell conductance.

30. A method of claim 28, wherein the pH sensitive potassium channel monomer polypeptide is recombinant.

31. A method of claim 28, wherein the pH sensitive potassium channel monomer polypeptide is mSlo3.

32. A method of claim 28, wherein the pH sensitive potassium channel monomer polypeptide is hSlo3.

33. A method of claim 28, wherein the pH sensitive potassium channel monomer polypeptide has an amino acid sequence of SEQ ID NO:1.

34. A method of claim 28, wherein the pH sensitive potassium channel monomer polypeptide has an amino acid sequence of SEQ ID NO:16 or SEQ ID NO:18.

35. A method of detecting the presence of Slo3 in mammalian tissue, the method comprising the steps of:

- (i) isolating a biological sample;
- (ii) contacting the biological sample with a Slo3-specific reagent
- 5 that selectively binds to Slo3; and,
- (iii) detecting the level of Slo3-specific reagent that selectively associates with the sample.

36. A method of claim 35, wherein the Slo3 specific reagent is selected from the group consisting of: Slo3 specific antibodies, Slo3 specific oligonucleotide primers, and Slo3 nucleic acid probes.

37. A method of claim 35, wherein the sample is from a human.

38. In a computer system, a method of screening for mutations of Slo3 genes, the method comprising the steps of:

- (i) receiving input of at least about 30 nucleotides of first nucleic acid sequence encoding a pH sensitive potassium channel protein having a nucleotide sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:17, or SEQ ID NO:19 and conservatively modified versions thereof;
- (ii) comparing the first nucleic acid sequence with a second nucleic acid sequence having substantial identity to the first nucleic acid sequence; and
- (iii) identifying nucleotide differences between the first and second nucleic acid sequences.

39. The method of claim 38, wherein the second nucleic acid sequence is associated with a disease state.

40. In a computer system, a method for identifying a three-dimensional structure of Slo3 proteins, the method comprising the steps of:

- (i) receiving input of at least about 10 amino acids of an amino acid sequence of a pH sensitive potassium channel monomer or at least about 30 nucleotides of a nucleotide sequence of a gene encoding the protein, the protein having an

amino acid sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:16, SEQ ID NO:18,
and conservatively modified versions thereof; and

(ii) generating a three-dimensional structure of the protein
encoded by the amino acid sequence.

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41. The method of claim 40, wherein said amino acid sequence is a
primary structure and wherein said generating step includes the steps of:

(i) forming a secondary structure from said primary structure using
energy terms encoded by the primary structure; and

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(ii) forming a tertiary structure from said secondary structure using
energy terms encoded by said secondary structure.

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42. The method of claim 40, wherein said generating step includes the
step of forming a quaternary structure from said tertiary structure using anisotropy terms
encoded by the tertiary structure.

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43. The method of claim 41, wherein said generating step further
includes the step of forming a quaternary structure from said tertiary structure using
anisotropy terms encoded by the tertiary structure.

44. The method of claim 40, further comprising the step of identifying
regions of the three-dimensional structure of the protein that bind to ligands and using the
regions to identify ligands that bind to the protein.

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SEQUENCE LISTING

mSlo3 amino acid sequence (SEQ ID NO:1):

MSQTLNLDLNLQKELTETSCTIEIQAAFILSSLATFFGGLIILFLFRIALKSSRSWKYVKGPRGLLELFSSRR
 5 IEANPLRKLYFHGVFRQRIEMLLSAQTVVGQVLVILVFLVLSIGSLVIYFINSMDPVRRCSSYEDKIVHGDLS
 FNAFFSFYFGLRFWAAEDKIKFWLEMNSIVDIFTIPPTFISYYLKSNNLGLRFLRALRLELPKILQILQVI
 KTSNSVKLSKLLSIVISTWFTAAGFLHLVENSQDPWLNGRNSQTMSYFESIYLVATMSTVGFQDVVAKTSL
 GRIFIVFFTLGSLILFANYIPEMVELFSTRKKYTKPYEAVKGKKFIVVCGNITVDSVTAFLRNFLHWKSGEI
 NIEIVFLGETLPCLELETLLKCHTSCNFCVGTALKFEDLKRVAVERSEACLILANHFCSLDLHEDNSNIMR
 10 VLSIKNYYPQTRVIIQILQSQNKVFLSKIIPNWDWSAGDNILCFABELKLGFIAGCLVPGLCTFLTTLFIEQN
 QKVFPKHPWQKHFLNGLKNKILTQRLSNDFVGMFTFPQVSRLCFVKLNLMIAIQHKPFFHSCCTLIILNPSSQ
 VRLNKDTLGGFIADSSKAVKRAFFYCSNCHSDVCNPELIGKCNCKIKSRQQLIAPTIMVKSSLTDFTTSSH
 IHASMSTEIHTCFSREQPSLITITTNRPPTNDTVDDTMDLSSGMFHWCRAMPLDKVVLKRSEKAKHEFQNH
 IVVCVFGDAQCTLVGLRNFMPLRASNYTRQELKDIVFIGSLEYFQREWRFLRNFPKIHIMPGSALYMGDLI
 15 AVNVEQSCMCVILATPYKALSSQILVDTEAIMATLNIQSLRITSPTPGSSKSEVKPSSAFDSKERKQRYKQI
 PILTELKNPSNIHFIEQMGGDLGMLKGTSLHLSTSFSTGAVFSDTFLDSLATSFYNYHVVELLQMLVTGGI
 SSEMEHYLVKEKPYKTTDDYEAIKSGRTRCKLGLLSLDQTVLSGINPRKTFGQLFCGSLDNFGILCVGLYRM
 IDEEPEPSQEHKRFVITRPSNECHLLPSDLVFCIIPFNTTCGKSDSSPFNRLKTTLQTRRRHWPRGRIR
 TMPTSPTIFTQSTTRERGGGLSTTTPELWTR

mSlo3 nucleotide sequence (SEQ ID NO:2):

ATGTCTCAAACATTGCTAGACAGTTTAAATCAGAAGGAGTTGACGGAAACGTCATGTACAATCGAAATCCAG
 GCAGCGTTTCATTCTTTCCTCCTTGGCGACTTTCTTCGGGGGACTCATCATCTTATTCCTTTTCAGAAATAGCC
 TTGAAAAGCTCAAGAAGTTGAAATACGTCAAGGGGCCAAGAGGACTCTTGAACTATTCTCATCACGTAGA
 25 ATCGAGGCTAATCCTTTGAGGAACTTTACTTTTCATGGAGTATTTTCGTCAGCGCATCGAAATGCTGCTTTCT
 GCACAGACCGTCGTGGGGCAAGTGTGGTGATCCTTGTCTTTGTACTAAGCATCGGGTCTCTTGTGATCTAT
 TTCATCAATTCAATGGATCCTGTTCTGAAGGTGTTCTTCATATGAAGACAAAATTGTCCATGGGGATTTGAGT
 TTCAACGCTTTCTTTAGCTTCTATTTTGGGTTGAGGTTTGGGCAGCTGAAGACAAGATCAAGTTCTGGTTG
 GAGATGAATTCAATTGTAGACATTTTTACCATCCCGCCAACCTTTATTTCTTATTATTGAAGAGTAATTGG
 30 CTAGGTTTGAGATTCTAAGAGCTCTGCGGTTGCTCGAACTCCCTAAAATCTTACAGATCCTACAAGTCATC
 AAGACCAGCAATTCAGTGAAGCTTTCCAAACTGTTGTCAATAGTTATCAGTACCTGGTTCACGGCAGCAGGA
 TTCCTTCACCTGGTGGAATACTCTGGTGACCCCTGGCTCAACGGAAGAACTCACAGACTATGTCATACTTT
 GAGTCTATTTATCTGGTGACAGCAACAATGTCAACTGTTGGCTTTGGGGACGTGGTGGCCAAGACATCCCTA
 GGACGGATTTTCATTGTTTTCTTCACCTTGGGAGTTTGATACTATTTGCAAACTACATTCCAGAAATGGTG
 35 GAGCTCTTTTCTACCAGGAAGAAATACCAAGCCCTACGAAGCAGTCAAAGGAAAAAAGTTCATCGTGGTC
 TGTGGAAACATCACAGTTGACAGTGTTACTGCTTTCTGAGGAATTTCTCCACTGGAAGTCCGGGGAAATC
 AATATTGAGATCGTATTCCTTGAGAGACTCTCCCTTGCTTGGAACTGGAGACCTTACTGAAGTGCCACACA
 TCCTGTACCAACTTCGTATGCGGCACCGCACTGAAGTTCGAGGATCTGAAGCGAGTTGCAGTGGAGAAGTCG
 GAGGCGTGCCTGATTCTAGCCAACCATTTCTGTAGTGACTTACATGACGAAGACAACCTCAAACATTATGAGG
 40 GTGCTCTCGATCAAGAACTATTATCCACAGACCAGAGTCATCATTACAGATACTTCAGTCTCAAAACAAGGTT

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TTCCTGTCAAAAATCCCCAACTGGGACTGGAGTGCTGGAGACAATATCCTCTGCTTTGCAGAGCTAAAGCTC
GGATTATATCGCCCAAGGCTGCTTGGTGCCAGGGCTGTGCACCTTTCTCACGACTCTGTTCATTGAACAAAAC
CAAAAAGTTTTTCTTAACATCCCTGGCAAAAACATTTCTTGAATGGCTTGAAGAACAAGATTCTGACACAG
CGCCTCTCTAACGACTTCGTGGGGATGACATTTCCCCAGGTCTCCCGGCTCTGCTTTGTGAAGCTAAATCTC
5 ATGCTGATCGCCATCCAACACAAGCCCTTCTTTCACAGTTGTTGCACTCTGATACTAAACCCATCATCCAA
GTGAGGCTGAATAAGGACACCTTAGGGTTCTTCATTGCGGACTCCTCCAAAGCCGTCAAAAGGGCTTTCTTT
TACTGTTCCAACGTGCACAGCGATGTGTGCAATCCTGAGCTAATTGGAAAGTGTAAGTGTAAAATCAAGAGC
CGACAACAACCTCATAGCACCGACCATCATGGTGATGAAAAGCAGCTTGACCGATTTACCACTTCTTCACAC
ATCCACGCTTCTATGTCAACAGAAATTCACACTTGTTTTTCAAGAGAACAGCCTAGTTTGATCACCATTACA
10 ACCAACAGACCAACGACAAACGACACAGTGGATGATACCGACATGCTGGACAGCAGTGGCATGTTTCACTGG
TGCAGAGCAATGCCCTTGGACAAGGTGGTTCTGAAACGAAGTGAGAAGGCAAAACACGAGTTTCAGAACCAC
ATTGTAGTATGCGTGTTTGGAGATGCCCAATGTACCCTGGTGGGGCTTCGGAATTTCTGTATGCCCTGAGA
GCCAGCAACTACACCCGGCAGGAGCTGAAGGACATTGTTTTTATTGGGTCTCTGGAGTACTTCCAGAGAGAA
TGGCGATTTCTCCGAAACTTTCCCAAGATACACATTATGCCTGGATCTGCACTCTACATGGGAGATCTGATT
15 GCAGTCAATGTAGAGCAGTGCTCTATGTGCGTCATCTTAGCCACACCCCTACAAGGCAGTGAAGCAGCCAGATT
CTGGTGGACACAGAGGCCATCATGGCCACCCTCAACATCCAGTCCCTGCGGATCACCAGTCCCTACTCCAGGG
TCTTCAAAGTCAGAAGTAAAGCCATCATCTGCCTTTGATAGTAAAGAAAGGAAGCAAAGATACAAACAGATC
CCCATTCTCACTGAAGTGAAGAATCCCTCCAACATCCACTTTATTGAGCAGATGGGCGGACTGGATGGAATG
CTCAAAGGGACTAGCTTGCATCTCAGCACTTCTTTCTCCACCGGTGCTGTCTTTTCAGACACCTTCTTGGAT
20 TCTCTCTGGCCACGTCTTCTACAATTACCATGTGCTGGAATTACTTCAGATGCTAGTGACTGGAGGCATA
AGCTCTGAGATGGAACACTATTTGGTTAAGGAGAAGCCCTATAAGACAACCTGACGACTATGAGGCAATCAAG
TCTGGGAGGACGCGGTGTAAGCTGGGACTCCTCTCTTTAGACCAAACCGTTCTATCAGGCATTAATCCAAGA
AAAACCTTTGGACAGCTGTTCTGTGGCTCATTGGATAATTTCCGGGATCCTATGTGTGGCTTATACCGTATG
ATTGATGAAGAGGAACCCAGCCAAGAACACAAAAGGTTTGTGATCACCAGGCCATCCAATGAGTGCCACCTG
25 CTGCCCTCAGATCTCGTGTTTTGTGCCATCCCTTTCAACACCACCTGTGGCAAATCAGACAGCAGTCCTTTC
AATTTCAAGGCTCAAAACAACCTCTACAAACGCGACGACGCCATTGGCCCAGGGGTGCAATTTCTTCGATTGCG
ACCATGCCGACGAGTCCCACGATCTTTACCCAGTCGACGACACGGGAGAGAGGTGGTCTCAGCACCACCACT
CCCAGTCTATCCTTTGGACACGTTAG

30 **hSlo3 amino acid sequence (SEQ ID NO:3):**

GLAALILSSFVTLFSLGLISLLIFRLIWRXVKWQIIKGTGIIILELFTSGTIARSHVRSLSLHFQGGFRDHIEML
LSAQTFVGQVLVILVFVLSIGSLIIYFINSADPVGTLFII

hSlo3 nucleotide sequence (SEQ ID NO:4):

35 GGCTTGGCAGCGCTCATTCTTTCCTCCTTTGTGACCCTCTTCAGTGGACTCATCAGCCTGTTGATCTTCAGG
CTGATCTGGAGAYCTGTAAAAAATGGCAAATCATCAAGGGAACAGGAATTATCTTGGAAGTTCACATCA
GGTACCATCGCTAGGAGCCATGTAAGAAGCCTCCACTTCCAGGGACAATTTCTGTGATCATATAGAAATGTTG
CTTTCAGCCCAGACCTTTGTGGGGCAAGTGTGGTGATCCTTGTCTTTGTACTAAGCATTGGGTCTCTTATA
ATCTATTTTCATCAATTCWGTGACCCTGTTGGAACGCTGTTTCATCATATGAAGACAAAACCATTCCTATTGA
40 TTTGGTTTTCAATGCTTTCTTTAGTTTCTATTTTGGGTTGAGGTTTTGGCAAAGCC

hSlo3-a amino acid sequence (SEQ ID NO:5)

GLAAFILSSFVTLFSGSLISLLIFRLIWRXVKKWQIIKGTGIILELFTSGTIARSHVRSLSLHFQGGFRDHIEML
LSAQTFVGQVLVILVFVLSIGSLIIYFINSADPVGTLFII

5

hSlo3-b amino acid sequence (SEQ ID NO:6)

GLAALILSSFVTLFTGLISLLIFRLIWRXVKKWQIIKGTGIILELFTSGTIARSHVRSLSLHFQGGFRDHIEML
LSAQTFVGQVLVILVFVLSIGSLIIYFINSADPVGTLFII

10 **hSlo3-c amino acid sequence (SEQ ID NO:7)**

GLAALILSSFVTLFSGSLISLLIFRLIWRXVKKWQIIKGTGIILELFTSGTIARSHVRSLSLHFQGGFRDHIEML
LSAQTFVGQVLVILVFVLSIGSLIIYFINSMDPVGTLFII

hSlo3-1 amino acid sequence (SEQ ID NO:16)

15 MFQTKLRNETWEDLPKMSCTTEIQAAFILSSFVTFSSGLIILLIFRLIWRXVKKWQIIKGTGIILELFTSGT
IARSHVRSLSLHFQGGFRDHIEMLLSAQTFVGQVLVILVFVLSIGSLIIYFINSADPVGSCSSYEDKTIPIDL
FNAFFSFYFGLRFMAADDKIKFWLEMNSIVDIFTIPPTFISYYLKSNNLGLRFLRALRLELPQILQILRAI
KTSNSVKFSKLLSIIILSTWFTAAGFIHLVENSGBPWLKGRNSQNI SYFESIYLMATTSTVGFGDVVAKTSL
GRTFIMFFTLGSLILFANYIPEMVELFANKRKYTSSYEALKGKKFIVVCGNITVDSVTAFLRNFLRDKSGEI
20 NTEIVFLGETPPSLELETIFKCYLAYTTFISGSAMKWEDLRRVAVESAEACLIIANPLCSDSHAEDISNIMR
VLSIKNYDSTTRIIIIQILQSHNKVYLPKIPSWNWDTGDNIIICFAELKLGFI AQGCLVPGLCTFLTSLFVEQN
KKVMPKQTKKKHFLNSMKNKILTQRLSDDFAGMSFPEVARLCFLKMYLLLLIAIEYKSLFTDGFGLILNPPP
QVRIRKNTLGFFIAETPKDVRRALFYCSVCHDDVFIPELITNCGCKSRSRQHITVPSVKRMKKCLKGISSRI
SGQDSPPRVSASTSSISNFTTRTLQHDVEQSDQDSSGMFHWCKPTSLDKVTLKRTGKSKYKFRNHIVACV
25 FGDAHSAPMGLRNFVMPLRASNYTRKELKDIVFIGSLDYLRQEWRFRLNFPQIYILPGCALYSGDLHAANIE
QCSMCAVLSPPPQPSSNQTLVDTEAIMATLTIGSLQIDSSSDPSVSEETPGYTNGHNEKSNCRKVPILTE
LKNPSNIHFIEQLGGLEGSLQETNLHLSTAFSTGTVFSSSFLLDLSLATAFYNYHVLELLQMLVTGGVSSQLE
QHLDKDKVYGVADSCSLLSGRNRCKLGLLSLHETILSDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDEEE
LNPENKRFVITRPA NEFKLLPSDLVFCAIPFSTACYKRNEEFSLQKSYEIVNKASQTTEDTFRHKLSSHPLI
30 QLLRHCIIHQSIILTSRELTPSLFLSK

hSlo3-1 nucleotide sequence (SEQ ID NO:17)

ATGTTTCAGACTAAGCTACGAAATGAACTTGGGAAGACTTGCCAAAAATGTCCTGCACAACCTGAGATCCAA
GCAGCATTCATTCTCTCTTCCTTTGTGACCTTCTTCAGTGGACTCATCATCCTGTTGATCTTCAGGCTGATC
35 TGGAGATCTGTAAAAAATGGCAAATCATCAAGGGAACAGGAATTATCTTGGAACCTGTTACATCAGGTACC
ATCGCTAGGAGCCATGTAAGAAGCCTCCACTTCCAGGGACAATTTTCGTGATCATATAGAAATGTTGCTTTCA
GCCCAGACCTTTGTGGGGCAAGTGTGGTGATCCTTGTCTTTGTACTAAGCATTGGGTCTCTTATAATCTAT
TTCATCAATTCTGCTGACCCTGTTGGAAGCTGTTTCATCATATGAAGACAAAACCATTCCTATTGATTTGGTT
TTCAATGCTTTCTTTAGTTTCTATTTTGGATTGAGGTTTATGGCAGCTGATGACAAGATCAAGTTCTGGCTG

GAGATGAATTCAATCGTAGACATCTTTACCATCCCACCAACCTTTATTTCTTATTATTTGAAGAGCAATTGG
 CTAGGTTTAAGGTTCCCTAAGAGCCTTGCGCCTGCTAGAACTCCCTCAAATCTTGCAAATCTACGAGCCATC
 AAGACCAGTAACCTCAGTGAAGTTTTCCAACTGCTGTCAATAATTCTCAGTACCTGGTTCACAGCTGCGGGA
 TTCATTACCTGGTGGAAAATTCTGGTGATCCCTGGCTCAAAGGTAGAAAATTCACAGAATATATCATATTTT
 5 GAGTCAATTTACCTGGTCAATGGCAACAACGTCAACCGTTGGATTGAGATGTGGTAGCCAAGACATCCTTA
 GGACGGACCTTCATCATGTTCTTCACACTGGGGAGTTTGATATTATTTGCGAACTATATACCTGAAATGGTG
 GAACTGTTTGCTAACAAGAGGAAATACACCAGTTCMTATGAAGCACTCAAAGGAAAGAAGTTTATTGTGGTC
 TGTGGAAACATCACTGTGGACAGTGTGACCGCTTTCTGAGGAATTTCTCCGCGACAAGTCAGGAGAGATC
 AACACTGAAATTGTTTTCTGGGAGAAACCCCTCCTTCTTTGGAACCTGAAACCATATTTAAATGCTACTTG
 10 GCCTACACAACGTTCAATTTCTGGATCTGCAATGAAGTGGGAGGATCTGAGGCGAGTTGCGGTGGAATCTGCA
 GAGGCATGCCTGATTATAGCCAATCCTTTGTGCAGTGATTCCCATGCTGAAGATATTTCCAACATTATGAGG
 GTGCTCTCTATCAAGAACTATGATTCTACCACCAGAATCATCATACAGATACTGCAATCCATAACAAGGTT
 TATCTGCCAAAGATTCCCAGCTGGAACGGGACACCGGAGACAACATCATCTGCTTTGCTGAATTAACACTT
 GGATTTATCGCCCAAGGCTGTTTGGTGCCAGGCTTGTGTACCTTCCTAACATCTCTATTTGTGGAGCAAAAC
 15 AAAAAAGGTTATGCCTAAACAGACCTGGAAGAAACACTTCTTGAATAGCATGAAAAACAAATTCTGACCCAA
 CGTCTCTCTGATGACTTTGCTGGAATGAGCTTTCTGAAGTTGCCCGGCTCTGCTTTCTGAAGATGTACCTC
 CTGTTGATAGCCATCGAATACAAGTCCCTCTTTACGGATGGTTTCTGTGGTCTGATACTAAATCCACCTCCA
 CAAGTGAGGATACGTAAGAACACATTAGGGTTCTTTATTGCTGAAACTCCAAAGGACGTGAGAAGAGCCTTG
 TTTTACTGTTTCACTGTGTCATGATGATGTGTTTCTTCTGAGCTAATTACAAACTGTGGCTGCAAAAGCAGA
 20 AGCCGGCAGCACATCACAGTGCCATCGGTAAAGAGAATGAAAAAATGTCTGAAGGGAATCTCCTCTCGTATA
 TCAGGGCAGGATTCTCCGCCAAGGGTATCTGCAAGCACTTCGAGCATATCAAACCTCACCACCAGGACTCTT
 CAACATGATGTAGAACAAGATTCTGACCAGCTTGATAGCAGTGGGATGTTTCACTGGTGCAAACCAACCTCT
 TTGGACAAGGTGACTCTGAAACGAACCTGGCAAGTCAAAGTATAAGTTTCGGAACCATATTGTAGCATGTGTA
 TTTGGAGATGCCCACTCAGCCCCGATGGGGCTTCGGAACCTTTGTAATGCCCTTGAGAGCCAGCAACTATACC
 25 AGGAAGGAGCTGAAGGACATAGTGTTCATTGGGTCTCTGGACTATCTACAGAGAGAATGGCGATTTCTCCGG
 AATTTTCCCAGATATACATTCTGCCTGGATGTGCACTTTATTCTGGAGACCTCCATGCGGCCAACATAGAG
 CAATGCTCCATGTGTGCTGTCTTGTCCCCCCCCACCCAGCCATCAAGCAACCAGACTTTGGTAGACACAGAA
 GCCATCATGGCAACCCTCACCATCGGATCCTTGCAAATTGACTCCTCCTCTGACCCGTCACCCTCAGTGTCA
 GAGGAGACTCCAGGTTACACAAATGGACATAATGAGAAATCAAACCTGCCGAAAAGTCCCTATCCTTACTGAA
 30 CTGAAAAATCCTTCCAACATTCACTTTATTGAACAGCTTGGTGGACTGGAAGGGTCCCTCCAAGAAACAAAT
 CTGCATCTCAGCACTGCCTTTTCTACGGGCACTGTTTTTCCAGCAGCTTCTTGGATTCTCTGCTGGCCACG
 GCCTTCTACAATTATCATGTCTCTGGAATTGCTTCAGATGCTGGTGACAGGAGGAGTAAGTTCTCAGCTGGAA
 CAACATTTAGATAAGGATAAAGTCTATGGTGTGGCAGATAGCTGCACGTCGCTCTTGTCTGGAAGAAACCGG
 TGTAAGCTGGGGCTTCTGTCTTACACGAAACCATTTTATCAGACGTTAATCCAAGAAACACCTTTGGACAA
 35 CTGTTCTGTGGCTCATTAGATCTTTTTGGAATCCTGTGTGTTGGCTTATACCGAATAATTGATGAAGAGGAG
 CTCAACCCAGAAAACAAAAGGTTTGTGATCACCCGGCCAGCCAATGAGTTCAAGCTGCTGCCTTCAGATCTT
 GTGTTTTGTGCCATACCCTTCAGCACTGCTTGTATAAAAGGAATGAAGAGTTCTCATTGCAAAAGTCATAT
 GAAATTGTAAATAAAGCATCACAGACAACAGAGGACACATTTCAGACACAAATTGTCTCCACCCATTGATT
 CAGTTACTGAGACATTGTATTCACCAGTCTATTCTTACCAGCCGAGAACTAACTCCCTCTCTTTTCTTAAGC
 40 AAATAGG

hSlo3-2 amino acid sequence (SEQ ID NO:18)

MFQTKLRNETWEDLPKMSCTTEIQAAFILSSSVTFFSGLIILLIFRLIWRSVKKWQIIKGTGIIILELFTSGT
IARSHVRSLSHFQGGFRDHIEMLLSAQTFVGQVLVILVFVLSIGSLIIYFINSADPVGSCSSYEDKTIPIDL
FNAFFSFYFGLRFMAADDKIKFWLEMNSIVDIFTIPPTFISYYLKSNNWLGLRFLRALRLELPQILQILRAI
5 KTSNSVKFSKLLSIILSTWFTAAGFIHLVENSGBPWLKGRNSQNI SYFESIYLMATTSTVGFGDVVAKTSL
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10 FYCSVCHDDVFIPELITNCGCKSRSRQHITVPSVKRMKKCLKGISSRISGQDSPPRVSASTSSISNFTTRTL
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LHLSTAFSTGTVFSSSFLDSSLATAFYNYHVLELLQMLVTGGVSSQLEQLDKDKVYGVADCTSLLSGRNR
15 CKLGLLSLHETILSDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDEEELNPENKRFVITRPA NEFKLLPSDL
VFCAIPFSTACYKRNEEFSLQKSYEIVNKASQTTEDTFRHKLSSHPLIQLLRHCIHQSI LTSRELTPSLFLS
K

hSlo-3-2 nucleotide sequence (SEQ ID NO:19)

20 ATGTTTCAGACTAAGCTACGAAATGAAACTTGGGAAGACTTGCCAAAAATGTCCTGCACA ACTGAGATCCAA
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GCCAGACCTTTGTGGGGCAAGTGTGGTGATCCTTGTCTTTGTACTAAGCATTGGGTCTCTTATAATCTAT
25 TTCATCAATTCTGCTGACCCTGTTGGAAGCTGTTTCATCATATGAAGACAAAACCATTCCATTGATTGTTGTT
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30 TTCATTACCTGGTGGAAAATTCTGGTGATCCCTGGCTCAAAGGTAGAAAATTCACAGAATATATCATATTTT
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35 AACACTGAAATTGTTTTCTGGGAGAAACCCCTCCTTCTTTGGAACCTGAAACCATATTTAAATGCTACTTG
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40 GGATTATCGCCCAAGGCTGTTTGGTGCCAGGCTTGTGTACCTTCCTAACATCTCTATTTGTGGAGCAAAAC

Sub

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25

AAAAAGGTTATGCCTAAACAGACCTGGAAGAAACACTTCTTGAATAGCATGAAAAACAAAATTCTGACCCAA
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